

Heps	RIVGGRDTSL	GRWPWQVSL.	....RYDG.A	HLCGGSLLSG	DWVLTAAHCF	PE....RNRV	LSRWRVFAGA	VAQASPHGLQ
Tadg15	RVVGGTDADE	GEWPWQVSL.	....HALGQG	HICGASLISP	NWLVSAAHCF	IDDRGFRYSD	PTQWTAFLGL	HDQSQRSAPG
Scce	KIIDGAPCAR	GSHPWQVAL.	....LSGNQL	H.CGGVLVNE	RWVLTAHCF.	.....K	MNEYTVHLGS	DTLG..DR.R
Try	KIVGGYNCEE	NSVPYQVSL.	....NSGYHF	..CGGSLINE	QWVVSAGHC.	.....Y	KSRIQVRLGE	HNIEVLEG.N
Chymb	RIVNGEDAVP	GSWPWQVSL.	....QDKTGF	HFCGGSLISE	DWVVTAAHC.	.....GV	RTSDVWVAGE	FDQGSDEE.N
Fac7	RIVGGKVCFK	GECPWQVLL.	....LVNG.A	QLCGGTLLINT	IKVVSAAHCF	.....AVLGE	HDLSEHDGDE	
Tpa	RIKGGLFADI	ASHPWQAAIF	AKHRRSPGER	FLCGGILISS	CWILSAAHCF	QERFPPHHL.	....TVILGR	.TYRVVFCEE

Heps	LGVQAVVYHG	GYLPFRDPNS	EENSNDIALV	HLSS.PLPLT	EYIQPVCLPA	...AGQALVD	GKICTVTGWG	NTQYYGQQ.A
Tadg15	VQERRLKRII	SHPPFNDFTF	D...YDIAL	ELEK.PAEYS	SMVRPICLPD	...ASHVFPA	GKAIWVTGWG	HTQYGGTG.A
Scce	AQRIKASKSF	RHPGYSTQT.	..HVNDMLV	KLNS.QARLS	SHVKKVRLPS	...RCE..PP	GTTCTVSGWG	TTTSPDVTFP
Try	EQFINAAKII	RHPQYDRKT.	..LNNDIMLI	KLSS.RAVIN	ARVSTISLPT	...APP..AT	GTKCLISGWG	NTASSGADYP
Chymb	IQVLKIAKVF	KMPKFSILT.	..VNNDITLL	KLAT.FARFS	QTVSAVCLPS	...ADDDFPA	GTLCAATTGWG	KTKYNANKTP
Fac7	QSRRAQVII	P....STYVP	GTTNHDIAL	RLHQ.FVVLT	DWVPLCLFE	RTFSERTLAF	VRFSLVSGWG	QLDRGATAL
Tpa	EQKFEVEKYI	VHKEFDDDTY	D...NDIAL	QLKSDSSRCA	QESSVVRTVC	LPPADLQLPD	WTECELSGYG	KHEALSPFYS

Heps	GVLQEARVPI	ISNDVCNGAD	FYGN..QIKP	KMFCAGYPEG	G.....IDA	CQGDSSGGPFV	CEDSISRTPR	WRLCGIVSWG
Tadg15	LILQKGEIRV	INQTTCE..N	LLPQ..QITP	RMMC VGFLSG	G.....VDS	CQGDSSGGPL.	..SSVEADGR	IFQAGVVSWG
Scce	SDLMCVDVKL	ISPQDCTKV.	.YKD..LLEN	SMLCAGIPDS	K.....KNA	CNGDSSGGPLV	C....R....	GTLOGLVSWG
Try	DELQCLDAPV	LSQAKCEAS.	.YPG..KITS	NMFCVGFLEG	G.....KDS	CQGDSSGGPVV	C....N....	GQLQGVVSWG
Chymb	DKLQQAALPL	LSNAECKKS.	.WGR..RITD	VMICAG..AS	G.....VSS	CMGDSSGGPLV	C....QKGA	WTLVGIVSWG
Fac7	ELMVLNVPR	MTQDCLQQR	XVGDSPNITE	YMFCAGYSDG	S.....KDS	CKGDSSGGP..	..HATHYRGT	WYLTGIVSWG
Tpa	ERLKEAHVRL	YPSSRCTSQH	LLNRT..VTD	NMLCAGDTRS	GGPQANLHDA	CQGDSSGGPLV	CLN...DGR	MTLVGIISWG

Heps	T.GCALAQKP	GVYTKVSDFR	EWIFQAIKTH	SEASGKNTQL	(SEQ ID NO:3)
Tadg15	D.GCAQRNKP	GVYTRLPLFR	DWIKENTGV	-----	(SEQ ID NO:3)
Scce	TFPCGQPNOP	GVYTQVCKFT	KWINDTMKKH	R-----	(SEQ ID NO:4)
Try	D.GCAQKNKP	GVYTKVYNYV	KWIKNTIAAN	S-----	(SEQ ID NO:5)
Chymb	SDTCS.TSSP	GVYARVTCLI	PWVQKILAN	-----	(SEQ ID NO:6)
Fac7	Q.GCATVGHF	GVYTRVSQYI	EWLQKLMRSE	PRPGVLLRAP	(SEQ ID NO:7)
Tpa	.LGCGQKDVP	GVYTKVTNYL	DWIRDNMRP	-----	(SEQ ID NO:8)

FIGURE 1

660207-ET221400

66027 E F F 2160

1 TCAAGAGCGGGCTCGGGGTACCATGGGAGCGATCGGGCCGCAAGGGCGGAGGGGGCCGAGGAGCTTGGGCGGGGACTCAAGTACAACCTCCCGGCAAGAGTGAATGGCTTGA  
M G S D R A R K G G G G P K D F G A G L K Y N S R E K V N G L E 33  
121 GGAAGCGGTGGAGTCTCTGCCAGTCAACAAGCTCAAGAAGGTGGAAGAGCATGGCCGGGGCGCTGGGTGGTCTGGCAGCGCGTGTATCGGCTCTCTGGTCTTGGGGATCGG  
E G V E F L P V N N V K K V E K E G P G R W V V L A A V L I G L L L V L L G I G 73  
241 CTCTCTGGTGTGGCATTTCAGTACCGGGAGCTGGTGTCCAGAAAGTCTTCAATGGCTACATGAGGATCACAATGAGAATTTTGGATGCTTACGAGAATCCAACTCCACTGAGTT  
F L V W H L Q Y R D V R V Q K V F N G Y M R I T N E N F V D A I E N S N S T E F 113  
361 TGTAAAGCTGGCCAGCAAGGTGAAGGACGGCTGAAGCTGCTGTACAGCGGAGTCCCATCTCTGGGGCCCTACCCAGGAGTGGCTGTGAGGGCTTCAGCGAGGGCAGGGCTCATCC  
V S L A S K V K D A L K L L Y S G V P F L G P Y H K E S A V T A F S E G S V I A 153  
481 CTACTACTGGTCTGAGTTGAGCATCCCGCAGCACCTGGTGGAGGAGCGCGGCGCTCATGGCCGAGGAGCGGGTAGTCATGCTGCCCGCGGGGGCGCTCCCTGAAGTCTTTGTGGT  
Y Y W S E F S I P Q H L V E E A E R V M A E R V M L P P R A R S L K S F V V 193  
601 CACCTCAGTGGTGGCTTTCCCGAGGACTCCAAACAGTACAGAGGAGCCAGGACACAGCTGCAGCTTTGGGCTGCAGCCCGGGGTGGAGCTGATGGCTTCACGAGCGCGGGCTT  
T S V V A F P T D S K T V Q R T Q D N S C S F G L H A R G V E L M R F T T P G F 233  
721 CCCTGACAGCGCTTACCGCTCATGGCGCTGCGAGTGGCGCTTGGGGGGGAGCGGAGTCTAGTCTGAGCGCTCACCTTCCGAGCTTTGAGCTTGGCTGCTGCGAGCGCGGGCAG  
P D S P Y P A H A R C Q W A L R G D A D S V L S L T F R S F D L A S C D E R G S 273  
841 CGAGCTGGTGAAGGTGTACACACCTGAGCGCCATGGAGCGCCAGCGCTGGTGCAGTTGTGTGGCACTACCTCCCTCTACACCTGAGCTTCCACTCTCCAGAGCTCTGCT  
D L V T V Y N T L S P M E P H A L V Q L C G T Y P P S Y N L T F H S S Q N V L L 313  
961 CATCACACTGATAACACTGAGCGCGGCTTGGAGGCACTTCTTCCAGTGGCTAGGATGAGCAGCTGTGGAGGGCGCTTGAAGCGGAGGAGGAGTCAACAG  
I T L I T N T E R R H P G F E A T F F Q L P R M S S C G G R L R K A Q G G T F N S 353  
1081 CCCTACTACCGAGGCACTACCCACCCCACTGAGTGCACATGGAACATTGAGGTGGCCCAACAGCAGTGTGAAGGTGAGCTTCAATCTCTTACTGCTGGAGCGCGGGCTGCC  
P Y Y P G H Y P P H I D C T W N I E V P N N Q H V K V S F K F F Y L L E P G V P 393  
1201 TGGGGGCACTCCCGCAAGGACTAGCTGGAGTCAATGGGAGAAATCTGGGAGAGAGTCCAGTGGTGGTGGTCCAGCAGCAACAGCAAGATCAAGTGGCTTCCACTGAGATCA  
A G T C P K D Y V E I N G E K Y C G E R S Q F V V T S N S N K I T V R F E S D Q 433  
1321 GTCTACACCGACCGGCTTCTTGAATACCTCTCTTACGATCCAGTCCAGCCATGCCCGGGGAGTTCAAGTGGCGCAGGGGGCGGTATCCGAGAGGAGTGGCTGGTGTATGG  
S Y T D T G F L A E Y L S Y D S S D P C P G F T C R T G R C I R K E L R C D G 473  
1441 CTGGGGGAGTGCACCGACCAAGGATGAGCTCAACTGCAGTGGGAGCGCGGCAACAGTTCAGCTGCAAGAACAGTTCGCAAGCGGCTCTCTGGGTCTGCGAGAGTGAACGA  
W A D C T D E S D E L N C S C D A G H Q F T C K N K F C K P L F W V C D S V N D 513  
1561 CTGGGAGACACAGCGAGGAGGAGGAGTGGTGTGGGCGCCAGAGCTTCAGGTGTTCATGGGAGTGGCTTGGAAAGCCAGCAGTGCATGGGAGGAGGAGTGTGGGAGCGG  
C G D N S D E Q G C S C P A Q T F R C S N G K C L S K S Q Q C H G K D D C G D G 553  
1681 GTCCGAGGAGGCTCTTGGCCCAAGGTGAAGCTGCTCACTTGTACCAACACACTACCGCTGGCTCAATGGGCTCTGCTTGAAGGAGGCAACCTGAGTGTGAGGGGAGGAGGAGT  
S D E A S C P K V N V V T C T K H T Y R C L N G L C L S K G N P E C D G K E D C 593  
1801 TAGCGAGCGCTCAGATGAGAAGGAGTGGGCTGAGTTCAGGAGACAGGCTGTGTGTGGGGGACCGGATGGGATGAGGGGAGTGGGCTGGCAGGTGAAGCTGCA  
S D G S D E K D C D C G L R S F T R Q A R V V G G T D A D E G E W P W Q V S L E 633  
1921 TGCTCTGGGCGAGGGCCACATCTGGGTGCTTCCCTCATCTCTCCCACTGGCTGGTCTCTGGCGCACACTGCTACATGATGACAGAGGATTCAAGTACTCAGACCCCGAGGAGTGGAC  
A L G Q G H I C G A S L I S P N W L V S A A E C Y I D D R G F R Y S D P T Q W T 673  
2041 GCGCTCTCTGGGCTTGCACAGCAGAGGAGCGGCGGCGGCTGGGGTGCAGGAGCGGAGGCTCAAGGCGCATCATCTCCACCGCTTCTTCAATGAGTTCAGCTTGGACTATGACATCGC  
A F L G L E D Q S Q R S A P G V Q E R R L K R I I S H P F F N D F T F D Y D I A 713  
2161 GCTGCTGGAGCTGGAGAAACCGGCGAGTACAGCTCCATGGTGGCGCCATCTGCTGCGGAGCGCTCCCATGTCTTCCCTGGCGGCAAGGCCACTGGGTCAAGGGCTGGGGACACAC  
L L E L E K P A E Y S S M V R P I C L P D A S H V F P A G K A I N V T G W G H T 753  
2281 CCAATATGGAGGCACTGGCGCGCTGATCTGCAAAAGGGTGAGATCCGCGTCATCAACAGGACCACTGCGAGAACCTCTGCGGAGGAGTCAAGCGCGGCTGATGTGGTGGGCTT  
Q Y G G T G A L I L Q K G E I R V I N Q T T C E N L L P Q Q I T P R M M C V G F 793  
2401 CCTCAGCGCGCGGCTGGAGTCTGCGAGGTGATTCGCGGGGACCCTGTCCAGCGTGGAGGCGGATGGGCGGATCTCCAGGCGGCTGTGGTGAAGTGGGAGAGCGGTGGCTCAGAG  
L S G G V D S C Q G D S G G P L S S V E A D G R I F Q A G V V S W G D G C A Q R 833  
2521 GAACAAGCCAGCGGTGTACAGAGGCTCCCTCTGTTTCGGGACTGGATCAAGAGAGAACACTGGGGTATAGGGGGCGGGCCACCCAAATGTACACTCTGGGGGCCACCCATGTGTCAC  
N K P G V Y T R L P L F R D W I K E N T G V (SEQ ID NO: 2) 855  
2641 CCCAGTGTGACCGCTGCGAGCTGGAGCTGGAGCGCTGACTGCACGAGCGCGCCAGAACATACACTGTGAATCAATCTCAGGGCTCCAAATCTGCTAGAAAACCTCTGCTCTCT  
2761 CAGCTCCAAAGTGGAGCTGGGAGTAGAAGGAGGAGCACTGGTGGTCTACTGAGCCCACTGGGGGCAAGGTTTGAAGACACAGCTCCCGGCGGAGCGGCAAGCTGGGGCGAGCGG  
2881 CGTTTGTGTATATCTGCTCCCGCTGTGTGAAGGAGCAGCGGAGCGGAGCTTCGAGCGCTCTCAGTGAAGGTTGGTGGGGCTGCGGGATCTGGGCTGTGGGGCGCTTGGGCGAGCTCT  
3001 TGAGGAAGCCAGGCTGGGAGGAGCTGGAAACAGAGCGGTCTGAGACTGAAATGTTTACCAGCTCCAGGGGTGGACTTCAGTGTGTGTTTGTGTAATGGGTAAAACATTTAT  
3121 TTCTTTTAAAAA (SEQ ID NO: 1)

FIGURE 2

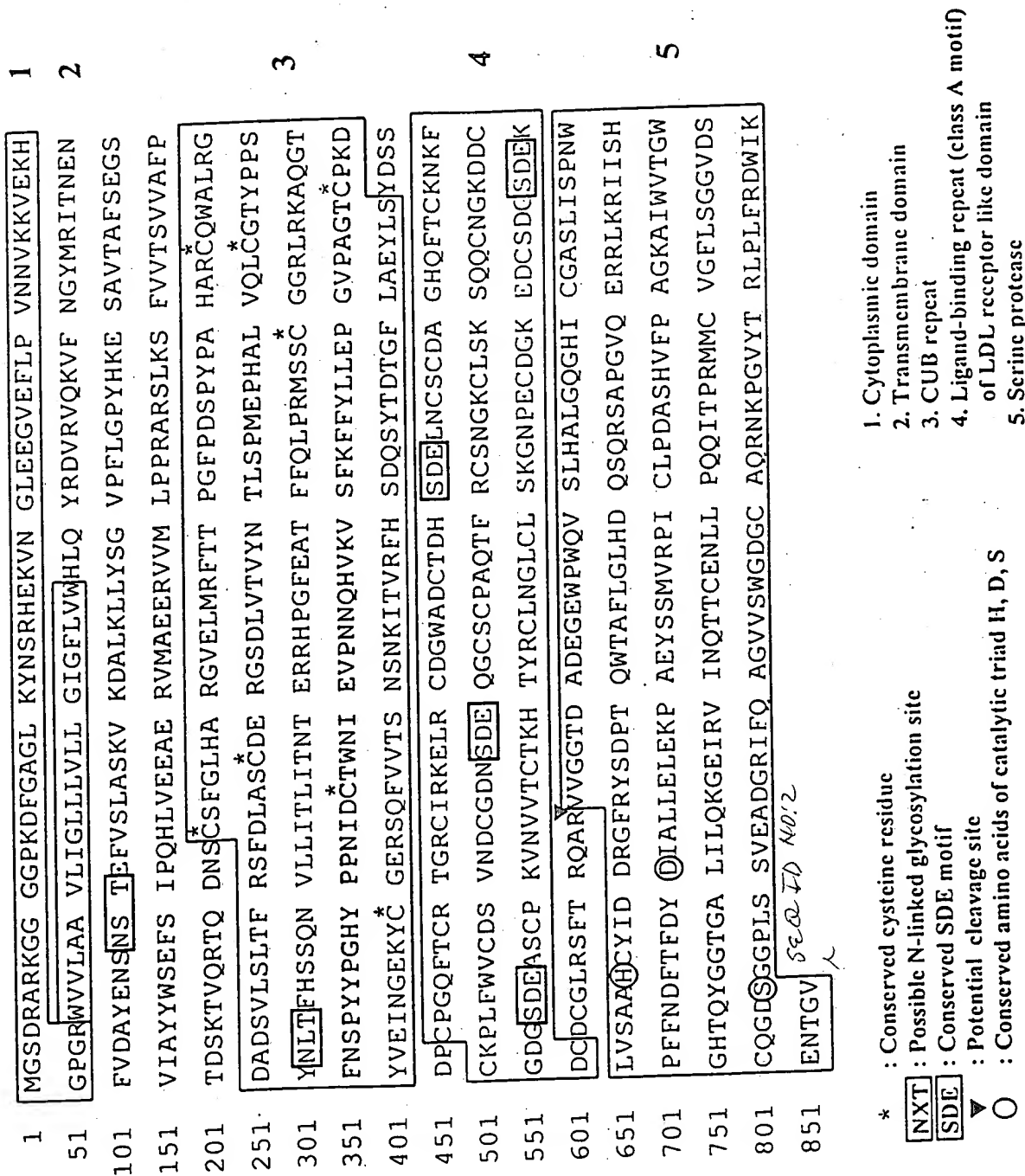


FIGURE 3

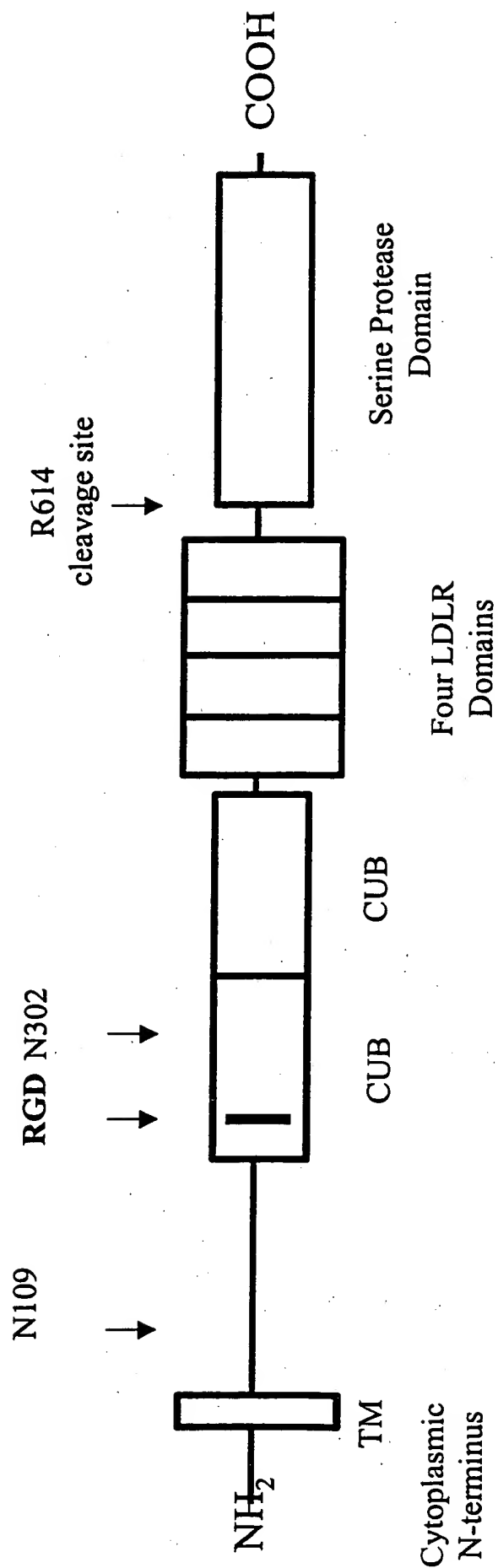


Figure 4

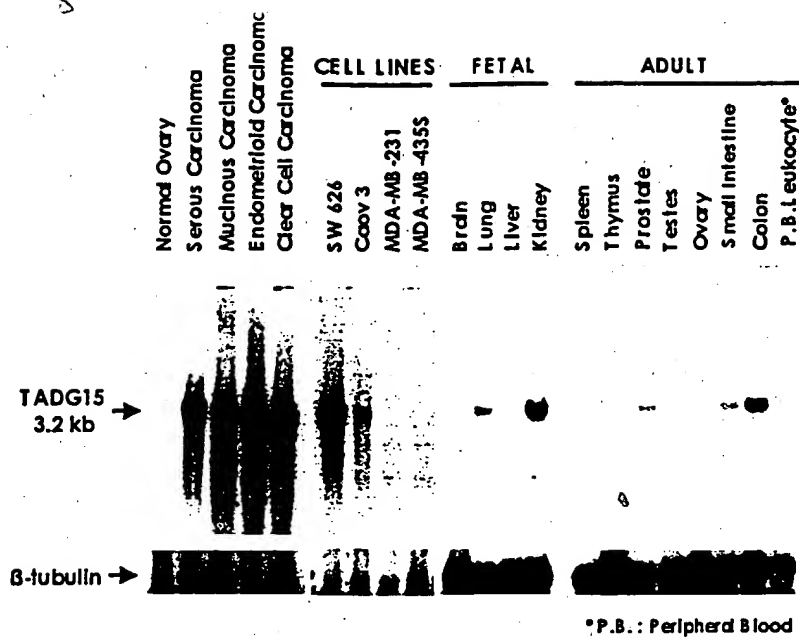
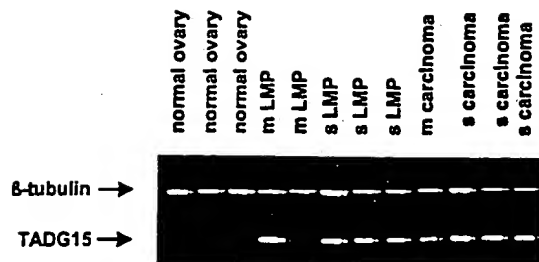


FIGURE 5

A



B

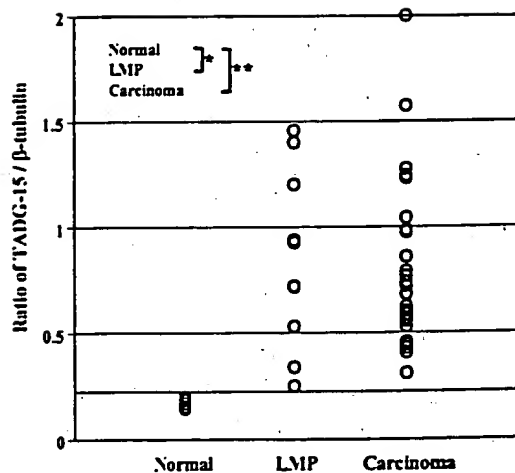


FIGURE 6

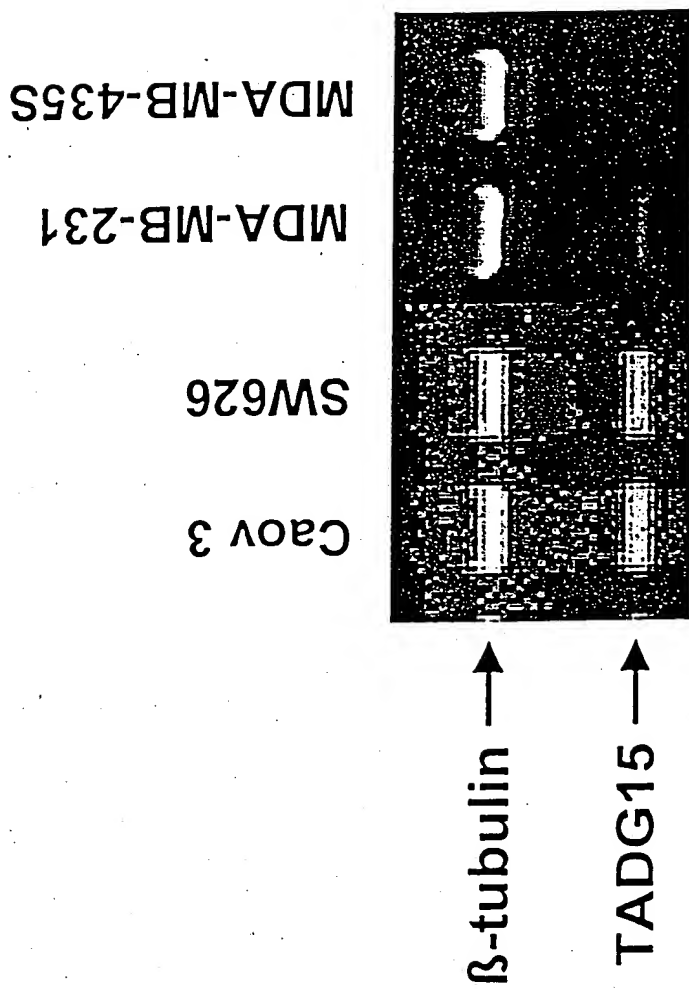


FIGURE 7

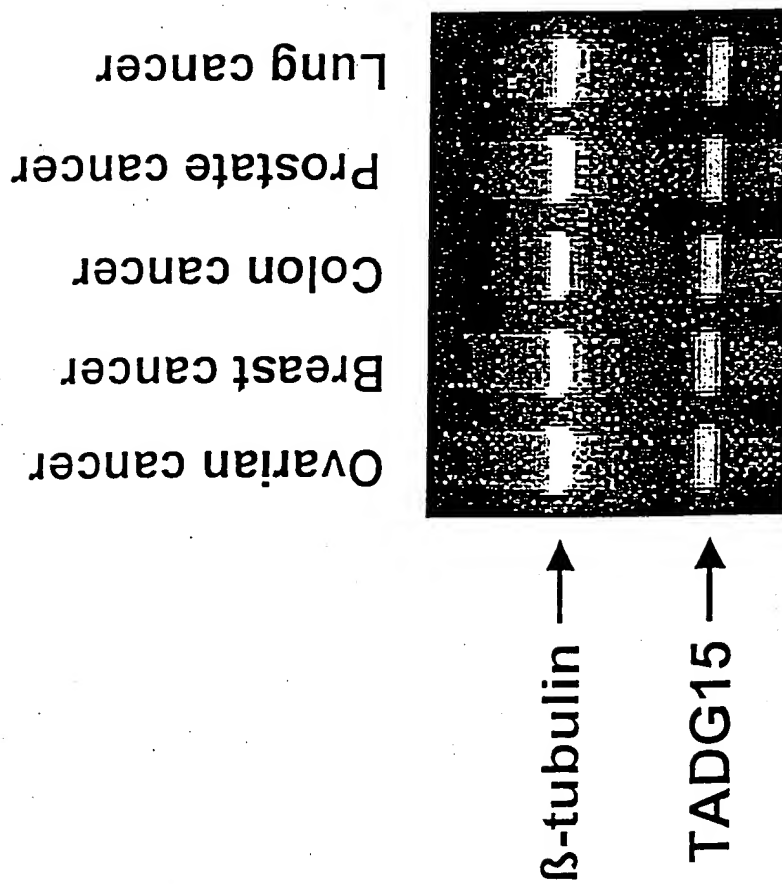


FIGURE 8



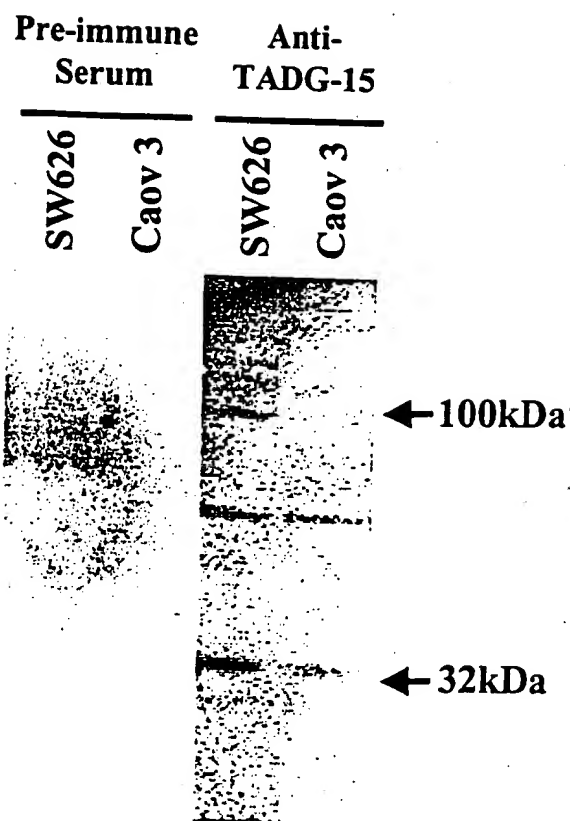


FIGURE 9

660201-FF2F2460

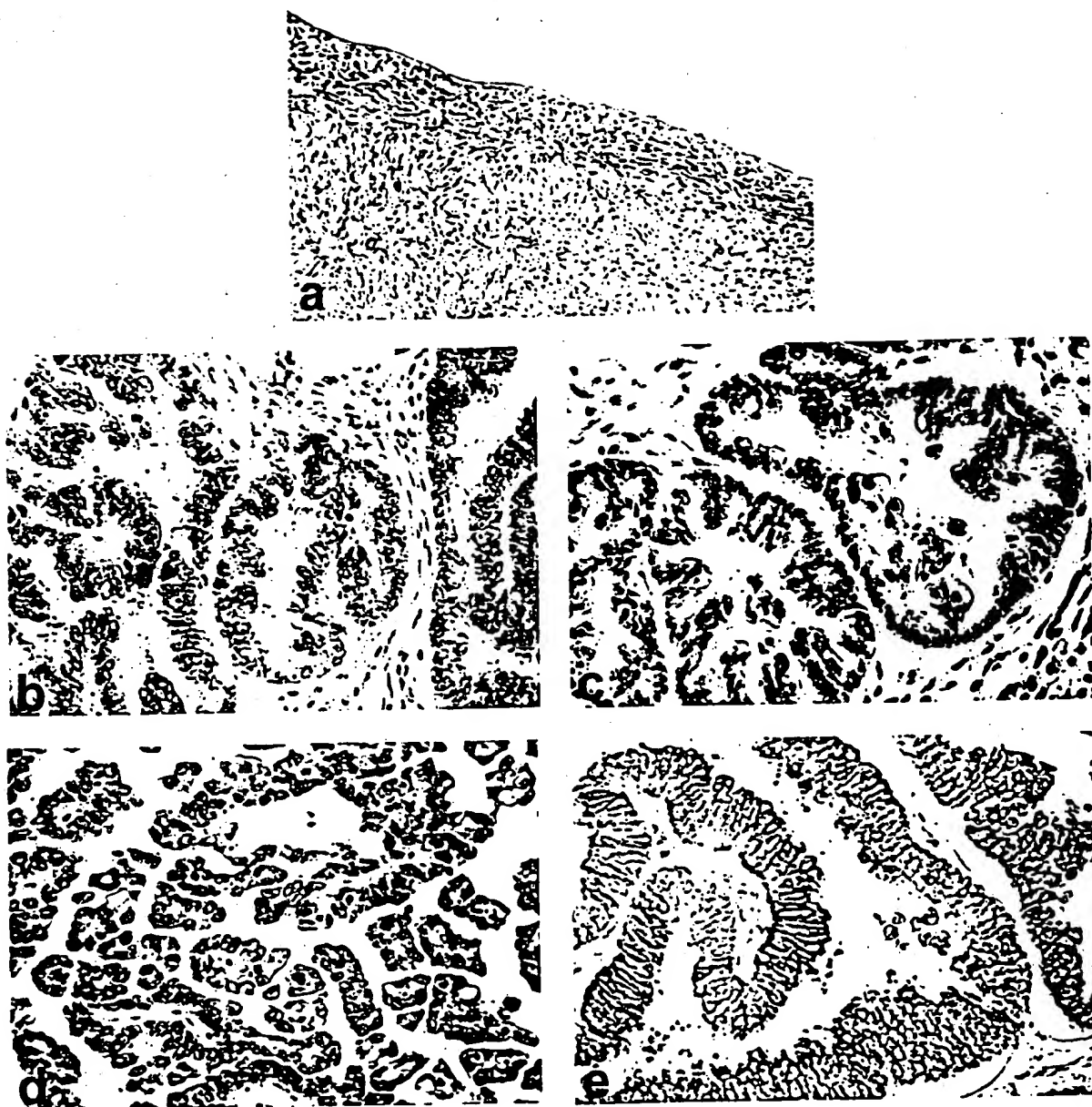


FIGURE 10

660207 E2E2400

htADG15	MGSDRARKGG	RDFFGAGL	KYNSRHEKVN	GLEEGVEFLF	VNVKKVEKH	50
mEpithin	---N-G--A-	--SQ-----	--D--L-NM-	-F-----	A--A-----R	
htADG15	GPGRWVVLAA	VLIGLLLVLL	GIGFLVWHLQ	YRDVRVQKVF	NGYMRITNEN	100
mEpithin	--R-----V-	--FSF--LS-	MA-L----FH	--N-----	--HL-----I	
htADG15	FVDAYENSNS	TEFVSLASKV	KDALKLLYSG	VPFLGPHYKE	SAVTAFSEGS	150
mEpithin	-L-----T-	---I---Q-	-E-----NE	--V-----K	-----	
htADG15	VIAYYWSEFS	IPQHLVEEAE	RVMAEERVVM	LPPRARSLSK	FVVTSVVAFP	200
mEpithin	-----	--P--A--VD	-A--V---T	-----A---	--L-----	
htADG15	TDSKTVQRTQ	DNSCSFGLHA	RGVELMRFTT	PGFPDSPYPA	HARCQWALRG	250
mEpithin	I-PRML----	-----A---	H-AAVT----	-----N---	-----V---	
htADG15	DADSVLSLTF	RSFDLASCDE	RGSDLVTVYN	TLSPMEPHAL	VQLCGTYPPS	300
mEpithin	-----	-----V-P---	H-----D	S-----V	-R---FS--	
htADG15	YNLTFHSSQN	VLLITLITNT	ERRHPGFEAT	FFQLPRMSSC	GGRLRKAQGT	350
mEpithin	-----L---	-F-V-----	G---L-----	-----K---	--V-SDT---	
htADG15	FNSPYYPGHY	PPNIDCTWNI	EVPNNQHVKV	SFKFFYLLEP	GVPAGTCPKD	400
mEpithin	-S-----	-----N---	K---RN---	R--L---VD-	N--V-S-T--	
htADG15	YVEINGEKYC	GERSQFVVTS	NSNKITVRFH	SDQSYTDTFG	LAEYLSYDSS	450
mEpithin	-----GS	-----S-	--S---H--	--H-----	-----N	
htADG15	DPCPGQFTCR	TGRCIRKELR	CDGWADCTDH	SDELNCSFDA	GHQFTCKNKF	500
mEpithin	-----M-M-K	-----	-----P-Y	---RY-R-N-	T-----Q-	
htADG15	CKPLFWVCDs	VNDCGDNSDE	QGCSCPAQTF	RCSNGKCLSK	SQQCNGKDDC	550
mEpithin	-----	-----G---	E-----GS-	K-----PQ	--K-----N-	
htADG15	GDGSDEASCP	KVNVVTCTKH	TYRCINGLCL	SKGNPECDGK	EDCSGDSDEK	600
mEpithin	-----D	S---S---Y	---Q-----	-----	T-----	
htADG15	DCDCGLRSFT	RQARVGGTD	ADEGEWPWQV	SLHALGQGHI	CGASLISPNW	650
mEpithin	N-----	K-----N	-----	-----L	-----D-	
htADG15	LVSAAHCIYID	DRGFRYSIPT	QWTAFLGLHD	QSQRSAPGVQ	ERRLKRIISH	700
mEpithin	-----FQ-	-KN-K---Y-	M-----L-	--K---S---	-LK-----T-	
htADG15	PFFNDFTFDY	DIALLELEKP	AEYSSMVRPI	CLPDASHVFP	AGKAIWVTGW	750
mEpithin	-S-----	-----S	V---TV---	-----T---	-----	
htADG15	GHTQYGGTGA	LILQKGEIRV	INQTTCEILL	PQQITPRMMC	VGFLSGGVDS	800
mEpithin	---KE-----	-----	-----D-M	-----	-----	
htADG15	CQGDSSGGPLS	SVEADGRIFQ	AGVVSXWGDGC	AQRNKPGVYT	RLPLFRDWIK	850
mEpithin	-----	-A-K---M--	-----E--	-----	---CSSGLDQ	
htADG15	ENTGV*	(SEQ ID NO:2)				900
mEpithin	RAHWGIAAWT	DSRPQTPTGM	PDMHTWIER	NTDDIYAVAS	PPQHNPDCEL	
htADG15	HP	(SEQ ID NO:10)				902
mEpithin	HP					

FIGURE 11

[illegible]

SNC19: .....

C

FIGURE 12-~~24~~

